

SEQUENCE LISTING

<110> Crane, Edmund H. III

<120> Maize Rar1 Interactor Polynucleotides
and Methods of Use

<130> 35718/262707

<150> 60/268,157

<151> 2001-02-12

<150> 10/074,473

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<160> 9

<170> FastSEQ for Windows Version 4.0

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<211> 691

<212> DNA

<213> Zea mays

<400> 1

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ctgacaatca tcgacagcgg cattggtatg accaagtcag acctgttgaa caaccttggg 240
accattgcgc ggtcaggcac gaaggaattc atggaggcac ttgctgctgg tgctgatgtg 300
tccatgattg gccagtttgg tgcgggttcc tactctgcct acctgttgac agagaggggt 360
gtcgtgacca ctaagcacia tgatgatgag cagtacgtgt gggagtctca ggctgggtgg 420
tccttctact tgcacagtga tacctctggg gagcaacttg gcaggggtac aaagatgacc 480
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<212> DNA

<213> Zea mays

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ttcgtcgacg acgacttcga gctggccacc gagctctaca gccaggccat cgacgccggg 180
cccgccaccg ccgacctcta tgccgaccgc gcccaggcgc acatcaagct cggcaactac 240
actgaggctg tggcggatgc taacaaagca attgagcttg atcctatgat gcataaagct 300
tactaccgga aaggtgctgc atgcattaag cttgaagaat accaaactgc aaaggctgct 360
cttgagttgg gttcttctta tgcacaggc gattcaagggt ttgctcgtct attgaaggaa 420
tgtgatgagc gcatcgctga ggaatctagc caggcaccag taaagaatgt tgaggctact 480
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atagaacccc caagcaaacc aaaatacagg c                                     571
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 <212> DNA
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 actaaagttt ggactgcccc tcttttgtaa atccagggtct tggaaactat gacctaatc 180
 tgcccaccca tagtgccatg agcttgcttg gttaagtctc tgcttttgta agctttctgt 240
 atgacagtct agcgtgtgtc tgagtgtctac ttgccgtagc ttttgatgga cataggtatg 300
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 <213> Zea mays

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 <222> (1)...(34)

<221> 3'UTR
 <222> (712)...(929)

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gca aag agc ggc tca gcc gca ccg gtg cgg tgc cag cgg atc ggc tgc 103
 Ala Lys Ser Gly Ser Ala Ala Pro Val Arg Cys Gln Arg Ile Gly Cys
 10 15 20

gac gcc gta ttc acc gac gat gac aac cgc gag ggc tcc tgc caa tac 151
 Asp Ala Val Phe Thr Asp Asp Asp Asn Arg Glu Gly Ser Cys Gln Tyr
 25 30 35

cac ccc tcc gca cct atg ttt cat gac ggc atg aaa gaa tgg agc tgc 199
 His Pro Ser Ala Pro Met Phe His Asp Gly Met Lys Glu Trp Ser Cys
 40 45 50 55

tgc aag caa aga agc cat gat ttc agc tta ttt ttg cag ata cct gga 247
 Cys Lys Gln Arg Ser His Asp Phe Ser Leu Phe Leu Gln Ile Pro Gly
 60 65 70

tgc aca aca gga aag cat aca acc gaa aaa cca atc aca aaa gct gtt 295
 Cys Thr Thr Gly Lys His Thr Thr Glu Lys Pro Ile Thr Lys Ala Val
 75 80 85

tca tct aac cgt aca aag gca aca ccg atc cag tcc tct aag cag ggt 343
 Ser Ser Asn Arg Thr Lys Ala Thr Pro Ile Gln Ser Ser Lys Gln Gly
 90 95 100

gtg gga gtt gat gtg tgt gca agg tgt cgt caa ggt ttc ttt tgc tcc 391
 Val Gly Val Asp Val Cys Ala Arg Cys Arg Gln Gly Phe Phe Cys Ser
 105 110 115
 gat cat gga tca cag ccc aag cca caa aag cca gct gct acc gac gat 439
 Asp His Gly Ser Gln Pro Lys Pro Gln Lys Pro Ala Ala Thr Asp Asp
 120 125 130 135
 aca aac aag gaa cct gtt gag aaa tca gct gtt cca ccg ccc aag aaa 487
 Thr Asn Lys Glu Pro Val Glu Lys Ser Ala Val Pro Pro Pro Lys Lys
 140 145 150
 agg atc gat gta aat gag ctg agg aca tgt aaa aat aaa gga tgt ggt 535
 Arg Ile Asp Val Asn Glu Leu Arg Thr Cys Lys Asn Lys Gly Cys Gly
 155 160 165
 aaa tcc tac aag gag aag gat aac cat gat tct gca tgt gac tac cat 583
 Lys Ser Tyr Lys Glu Lys Asp Asn His Asp Ser Ala Cys Asp Tyr His
 170 175 180
 cca ggt cct gcc gtt ttc cat gac agg atg aga ggg tgg aaa tgc tgt 631
 Pro Gly Pro Ala Val Phe His Asp Arg Met Arg Gly Trp Lys Cys Cys
 185 190 195
 gat gtt cat gtc aag gag ttt gac gag ttt atg gag ata cct aca tgc 679
 Asp Val His Val Lys Glu Phe Asp Glu Phe Met Glu Ile Pro Thr Cys
 200 205 210 215
 aca aag ggt tgg cat aat gct gat gcg gtg tgaattcacc ccatgcttaa 729
 Thr Lys Gly Trp His Asn Ala Asp Ala Val
 220 225
 ggctgttttc atgttgtatc gtcacctgcc atgtaaacac catttctgca gttcattgag 789
 gatttcattt ggaagtgtga caagagcttt gaggacgggc tgcctaagct ttgcgcacgg 849
 tagctgtctg gaaatcttac gtgattctcc ttgcacattt ggtgtctgga tttaaattgg 909
 ggttttgtct gtttgaagcc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 969
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1008

<210> 5
 <211> 225
 <212> PRT
 <213> Zea mays

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 Arg Glu Gly Ser Cys Gln Tyr His Pro Ser Ala Pro Met Phe His Asp
 35 40 45
 Gly Met Lys Glu Trp Ser Cys Cys Lys Gln Arg Ser His Asp Phe Ser
 50 55 60
 Leu Phe Leu Gln Ile Pro Gly Cys Thr Thr Gly Lys His Thr Thr Glu
 65 70 75 80
 Lys Pro Ile Thr Lys Ala Val Ser Ser Asn Arg Thr Lys Ala Thr Pro
 85 90 95

Ile Gln Ser Ser Lys Gln Gly Val Gly Val Asp Val Cys Ala Arg Cys
 100 105 110
 Arg Gln Gly Phe Phe Cys Ser Asp His Gly Ser Gln Pro Lys Pro Gln
 115 120 125
 Lys Pro Ala Ala Thr Asp Asp Thr Asn Lys Glu Pro Val Glu Lys Ser
 130 135 140
 Ala Val Pro Pro Pro Lys Lys Arg Ile Asp Val Asn Glu Leu Arg Thr
 145 150 155 160
 Cys Lys Asn Lys Gly Cys Gly Lys Ser Tyr Lys Glu Lys Asp Asn His
 165 170 175
 Asp Ser Ala Cys Asp Tyr His Pro Gly Pro Ala Val Phe His Asp Arg
 180 185 190
 Met Arg Gly Trp Lys Cys Cys Asp Val His Val Lys Glu Phe Asp Glu
 195 200 205
 Phe Met Glu Ile Pro Thr Cys Thr Lys Gly Trp His Asn Ala Asp Ala
 210 215 220
 Val
 225

<210> 6
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide based upon an adaptor
 used for cDNA library construction and poly(dT) to
 remove clones which have a poly(A) tail but no
 cDNA insert.

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<210> 7
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 <212> DNA
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<220>
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 Met Ala Ala Ser Asp Leu Glu Ser Lys Ala
 1 5 10

 aag gag gcc ttc gtc gac gac gac ttc gag ctg gcc acc gag ctc tac 159
 Lys Glu Ala Phe Val Asp Asp Asp Phe Glu Leu Ala Thr Glu Leu Tyr
 15 20 25

 agc cag gcc atc gac gcc ggg ccc gcc acc gcc gac ctc tat gcc gac 207
 Ser Gln Ala Ile Asp Ala Gly Pro Ala Thr Ala Asp Leu Tyr Ala Asp
 30 35 40

cg	gc	ca	gc	ca	at	aa	ct	gg	aa	ta	ac	ga	gc	gt	gc	255
Arg	Ala	Gln	Ala	His	Ile	Lys	Leu	Gly	Asn	Tyr	Thr	Glu	Ala	Val	Ala	
		45					50					55				
ga	gc	aa	aa	gc	at	ga	ct	ga	cc	at	at	ca	aa	gc	ta	303
Asp	Ala	Asn	Lys	Ala	Ile	Glu	Leu	Asp	Pro	Met	Met	His	Lys	Ala	Tyr	
	60					65				70						
ta	cg	aa	gg	gc	tg	at	aa	ct	ga	ga	ta	ca	ac	gc	351	
Tyr	Arg	Lys	Gly	Ala	Ala	Cys	Ile	Lys	Leu	Glu	Glu	Tyr	Gln	Thr	Ala	
	75			80					85			90				
aa	gc	gc	ct	ga	tt	gg	tc	tc	ta	gc	tc	gg	ga	tc	ag	399
Lys	Ala	Ala	Leu	Glu	Leu	Gly	Ser	Ser	Tyr	Ala	Ser	Gly	Asp	Ser	Arg	
			95						100					105		
tt	gc	cg	ct	tt	aa	ga	tg	ga	ga	cg	at	gc	ga	ga	tc	447
Phe	Ala	Arg	Leu	Leu	Lys	Glu	Cys	Asp	Glu	Arg	Ile	Ala	Glu	Glu	Ser	
			110					115					120			
ag	ca	gc	cc	gt	aa	aa	gt	ga	gc	ac	gt	gc	gc	ac	at	495
Ser	Gln	Ala	Pro	Val	Lys	Asn	Val	Glu	Ala	Thr	Val	Ala	Ala	Thr	Ile	
		125					130					135				
ga	gc	aa	ga	ga	tt	ac	aa	at	ga	aa	ac	cc	cc	gt	at	543
Glu	Asp	Lys	Glu	Asp	Phe	Thr	Asn	Met	Glu	Asn	Thr	Pro	Pro	Val	Ile	
	140					145					150					
ga	cc	cc	ag	aa	cc	aa	ta	ag	ca	ga	ta	ta	aa	ag	gc	591
Glu	Pro	Pro	Ser	Lys	Pro	Lys	Tyr	Arg	His	Asp	Tyr	Tyr	Asn	Ser	Ala	
	155				160					165					170	
ac	ga	gt	gt	ct	ac	at	tt	gc	aa	gg	gt	cc	gc	ga	ag	639
Thr	Glu	Val	Val	Leu	Thr	Ile	Phe	Ala	Lys	Gly	Val	Pro	Ala	Asp	Ser	
			175					180						185		
gt	gc	at	ga	tt	gg	ga	ca	at	tt	ag	gt	ta	cc	at	ga	687
Val	Val	Ile	Asp	Phe	Gly	Glu	Gln	Met	Leu	Ser	Val	Ser	Ile	Glu	Val	
			190					195					200			
cc	gg	ga	ga	cc	ta	ca	tt	ca	cc	cg	ct	tt	tc	aa	at	735
Pro	Gly	Glu	Glu	Pro	Tyr	His	Phe	Gln	Pro	Arg	Leu	Phe	Ser	Lys	Ile	
		205					210					215				
at	cc	ga	aa	tg	aa	ta	ca	gc	ta	cc	ac	aa	gt	ga	at	783
Ile	Pro	Glu	Lys	Cys	Lys	Tyr	Gln	Val	Leu	Ser	Thr	Lys	Val	Glu	Ile	
	220					225					230					
cg	ct	gc	aa	gc	ga	ca	gt	ac	tg	ac	ac	ct	ga	ta	ag	831
Arg	Leu	Ala	Lys	Ala	Glu	Gln	Val	Thr	Trp	Thr	Thr	Leu	Asp	Tyr	Ser	
	235				240					245					250	
gg	ag	cc	aa	ac	gt	cc	ca	aa	at	ag	ac	cc	gc	ga	ac	879
Gly	Arg	Pro	Lys	Thr	Val	Pro	Gln	Lys	Ile	Ser	Thr	Pro	Ala	Glu	Thr	
			255					260						265		

gcc cca aga cct tca tac cca tct tca aag gcg aaa aaa gac tgg gat 927
 Ala Pro Arg Pro Ser Tyr Pro Ser Ser Lys Ala Lys Lys Asp Trp Asp
 270 275 280

aaa ctg gaa gct gaa gtc aaa aag gag gag aag gaa gaa aaa ctt gat 975
 Lys Leu Glu Ala Glu Val Lys Lys Glu Glu Lys Glu Glu Lys Leu Asp
 285 290 295

ggg gat gct gca ttg aac aaa ttc ttc cgt gac atc tac aag gat gct 1023
 Gly Asp Ala Ala Leu Asn Lys Phe Phe Arg Asp Ile Tyr Lys Asp Ala
 300 305 310

gat gaa gat atg cgg agg gcc atg atg aag tca ttc gtg gaa tca aat 1071
 Asp Glu Asp Met Arg Arg Ala Met Met Lys Ser Phe Val Glu Ser Asn
 315 320 325 330

ggc act gtt ctc tca acc aat tgg aaa gat gtt gga gca aag aag gta 1119
 Gly Thr Val Leu Ser Thr Asn Trp Lys Asp Val Gly Ala Lys Lys Val
 335 340 345

gaa ggg agc ccc cct gat ggt atg gag ctc aag aag tgg gaa tac taa 1167
 Glu Gly Ser Pro Pro Asp Gly Met Glu Leu Lys Lys Trp Glu Tyr *
 350 355 360

agtttggact gcccgctctt tgtaaatcca ggtcttggaa actatgacct aattctgccc 1227
 acccatagtg ccatgagctt gcttggttaa gtctctgctt ttgtaagctt tctgtatgac 1287
 agtctagcgt gtgtctgagt gctacttgcc gtagcttttg atggacatag gtatgctatt 1347
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<210> 8
 <211> 361
 <212> PRT
 <213> Zea mays

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 Gly Pro Ala Thr Ala Asp Leu Tyr Ala Asp Arg Ala Gln Ala His Ile
 35 40 45
 Lys Leu Gly Asn Tyr Thr Glu Ala Val Ala Asp Ala Asn Lys Ala Ile
 50 55 60
 Glu Leu Asp Pro Met Met His Lys Ala Tyr Tyr Arg Lys Gly Ala Ala
 65 70 75 80
 Cys Ile Lys Leu Glu Glu Tyr Gln Thr Ala Lys Ala Ala Leu Glu Leu
 85 90 95
 Gly Ser Ser Tyr Ala Ser Gly Asp Ser Arg Phe Ala Arg Leu Leu Lys
 100 105 110
 Glu Cys Asp Glu Arg Ile Ala Glu Glu Ser Ser Gln Ala Pro Val Lys
 115 120 125
 Asn Val Glu Ala Thr Val Ala Ala Thr Ile Glu Asp Lys Glu Asp Phe
 130 135 140
 Thr Asn Met Glu Asn Thr Pro Pro Val Ile Glu Pro Pro Ser Lys Pro
 145 150 155 160
 Lys Tyr Arg His Asp Tyr Tyr Asn Ser Ala Thr Glu Val Val Leu Thr

tgc att aag ctt gaa gaa tac caa act gca aag gct gct ctt gag ttg	288
Cys Ile Lys Leu Glu Glu Tyr Gln Thr Ala Lys Ala Ala Leu Glu Leu	
85 90 95	
ggg tct tct tat gca tca ggc gat tca agg ttt gct cgt cta ttg aag	336
Gly Ser Ser Tyr Ala Ser Gly Asp Ser Arg Phe Ala Arg Leu Leu Lys	
100 105 110	
gaa tgt gat gag cgc atc gct gag gaa tct agc cag gca cca gta aag	384
Glu Cys Asp Glu Arg Ile Ala Glu Glu Ser Ser Gln Ala Pro Val Lys	
115 120 125	
aat gtt gag gct act gtg gct gct act att gag gac aag gag gat ttc	432
Asn Val Glu Ala Thr Val Ala Ala Thr Ile Glu Asp Lys Glu Asp Phe	
130 135 140	
aca aat atg gag aat aca cca cca gtg ata gaa ccc cca agc aaa cca	480
Thr Asn Met Glu Asn Thr Pro Pro Val Ile Glu Pro Pro Ser Lys Pro	
145 150 155 160	
aaa tac agg cat gac tac tac aac agt gcc aca gaa gtg gta ctg aca	528
Lys Tyr Arg His Asp Tyr Tyr Asn Ser Ala Thr Glu Val Val Leu Thr	
165 170 175	
ata ttt gct aag ggt gtt cct gct gat agt gta gtc att gat ttt ggt	576
Ile Phe Ala Lys Gly Val Pro Ala Asp Ser Val Val Ile Asp Phe Gly	
180 185 190	
gaa cag atg ttg agt gta tcc att gaa gtt cct ggt gaa gaa cca tac	624
Glu Gln Met Leu Ser Val Ser Ile Glu Val Pro Gly Glu Glu Pro Tyr	
195 200 205	
cat ttt cag ccc cgt ctg ttt tct aag att atc cct gag aaa tgc aaa	672
His Phe Gln Pro Arg Leu Phe Ser Lys Ile Ile Pro Glu Lys Cys Lys	
210 215 220	
tat caa gtc tta tcc acc aag gtt gaa ata cgc ctt gca aaa gct gag	720
Tyr Gln Val Leu Ser Thr Lys Val Glu Ile Arg Leu Ala Lys Ala Glu	
225 230 235 240	
cag gtg aca tgg aca acc ctg gat tat agt gga aga cca aag act gtt	768
Gln Val Thr Trp Thr Thr Leu Asp Tyr Ser Gly Arg Pro Lys Thr Val	
245 250 255	
ccc cag aag ata agc acg cca gct gaa aca gcc cca aga cct tca tac	816
Pro Gln Lys Ile Ser Thr Pro Ala Glu Thr Ala Pro Arg Pro Ser Tyr	
260 265 270	
cca tct tca aag gcg aaa aaa gac tgg gat aaa ctg gaa gct gaa gtc	864
Pro Ser Ser Lys Ala Lys Lys Asp Trp Asp Lys Leu Glu Ala Glu Val	
275 280 285	
aaa aag gag gag aag gaa gaa aaa ctt gat ggt gat gct gca ttg aac	912
Lys Lys Glu Glu Lys Glu Glu Lys Leu Asp Gly Asp Ala Ala Leu Asn	
290 295 300	
aaa ttc ttc cgt gac atc tac aag gat gct gat gaa gat atg cgg agg	960

Lys Phe Phe Arg Asp Ile Tyr Lys Asp Ala Asp Glu Asp Met Arg Arg
 305 310 315 320

gcc atg atg aag tca ttc gtg gaa tca aat ggc act gtt ctc tca acc 1008
 Ala Met Met Lys Ser Phe Val Glu Ser Asn Gly Thr Val Leu Ser Thr
 325 330 335

aat tgg aaa gat gtt gga gca aag aag gta gaa ggg agc ccc cct gat 1056
 Asn Trp Lys Asp Val Gly Ala Lys Lys Val Glu Gly Ser Pro Pro Asp
 340 345 350

ggt atg gag ctc aag aag tgg gaa tac taa 1086
 Gly Met Glu Leu Lys Lys Trp Glu Tyr *
 355 360